



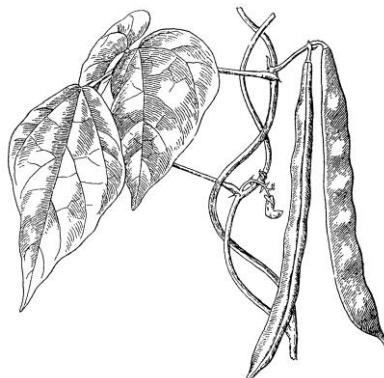
Hrvatska zaklada za znanost



# Podrijetlo, udomaćenje i širenje graha (*Phaseolus vulgaris* L.)

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Zagreb, 11. lipnja 2015.



- rod *Phaseolus* sadržava 70-tak vrsta podrijetlom iz Centralne i Sjeverne Amerike

- pet vrsta je udomaćeno:



*P. vulgaris*



*P. acutifolius*



*P. dumosus*

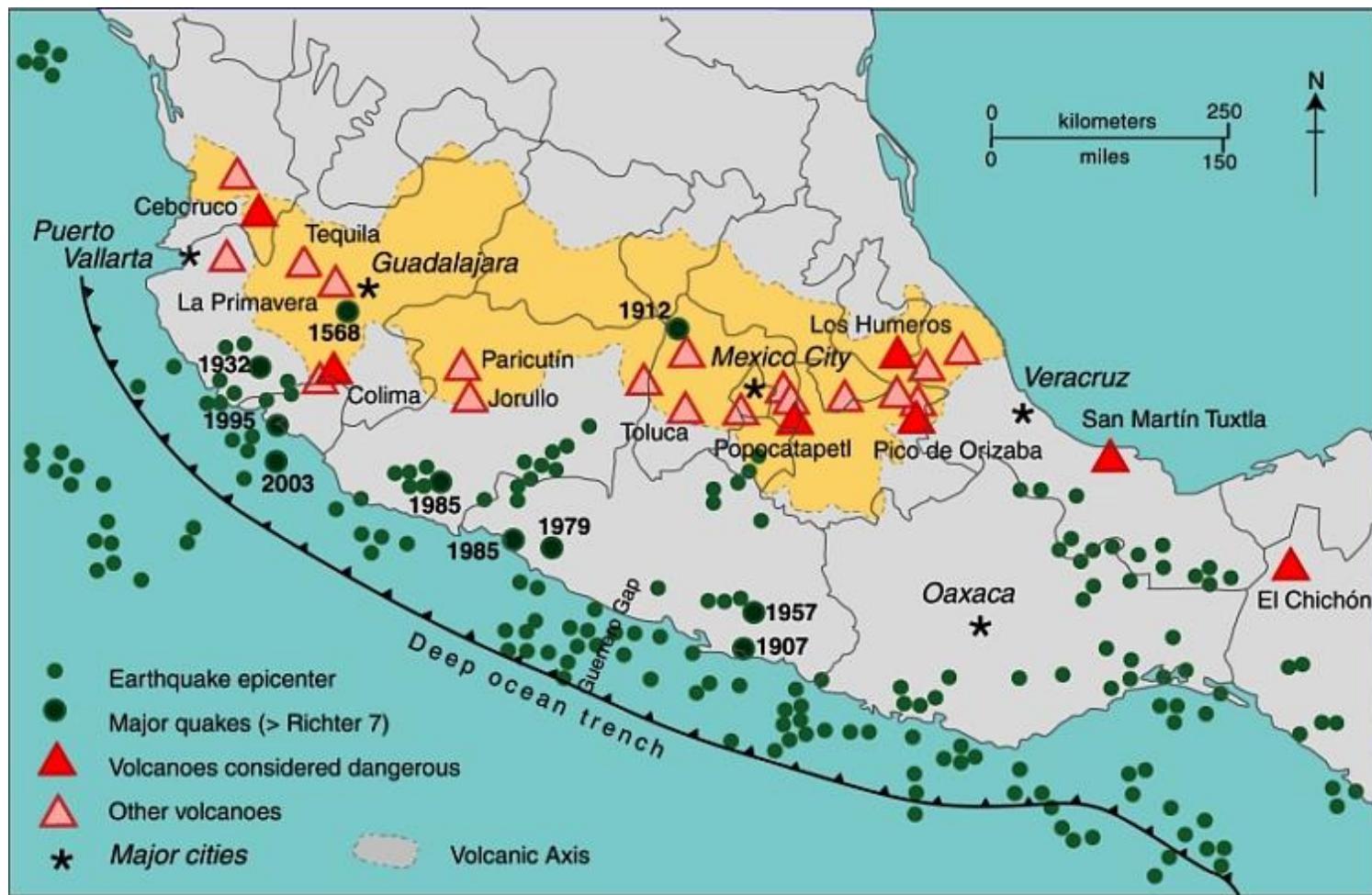


*P. lunatus*



*P. coccineus*

- sekvenciranje unutarnje transkribirajuće razmagnice ribosomalne DNA (ITS) i kloroplastnog *trnK* lokusa (*Delgado-Salinas et al. 2006*) su omogućili datiranje roda na ca. 4–6 milijuna godina.

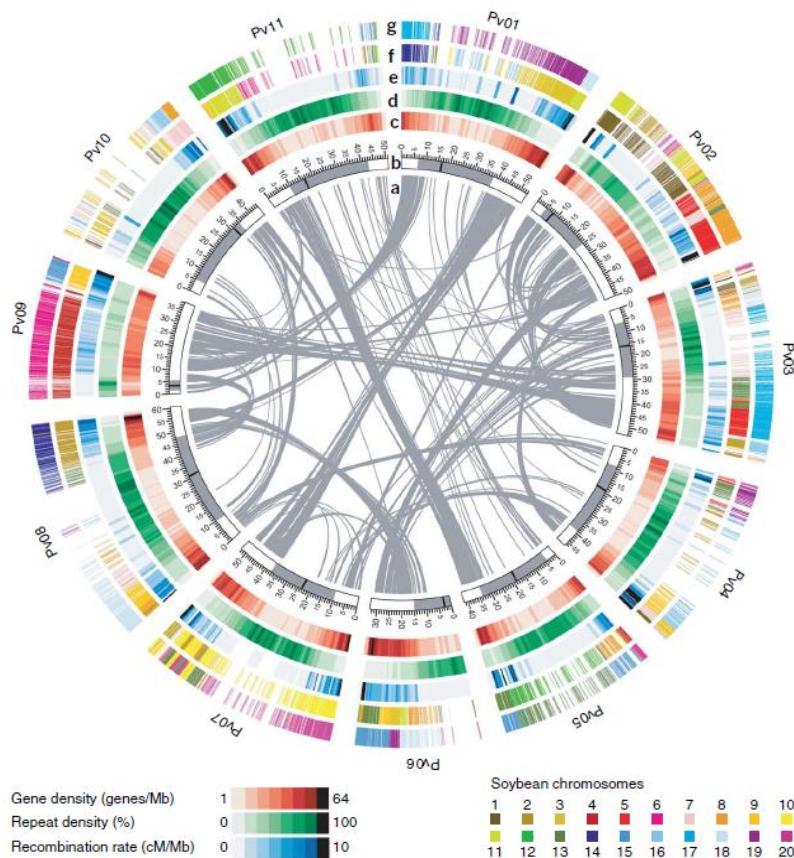


- obični grah (Phaseolus vulgaris L.) ( $2n = 22$ )



~ 600 Mb, 27197 proteinski gen (Schmutz i sur. 2014)

- 91% proteinskih gena dijeli sa sojom



Struktura genoma graha i sintenija s genomom soje (Schmutz i sur 2014)

- za efikasnu zaštitu i upotrebu germplazme u razvoju novih poboljšanih kultivara izuzetno je važno istraživanje podrijetla i evolucije vrste



- divlji grah potječe iz Srednje Amerike (*Bittochi i sur. 2012, Schmutz i sur. 2014*)

- rasprostranjenje od Meksika do Argentine s dva eko-geografska genska skupa (djelomično reproduktivno izolirani)

- za andske divlje populacije je zabilježen višestruki prolazak kroz genetičko usko grlo (*Kwak and Gepts 2009, Rossi i sur. 2009*)

- udomaćenje se odvijalo istovremeno na dvije lokacije što je jedinstven scenarij kod kultiviranih biljaka (*Gaut 2014*)



### Milpa cropping system

- udomaćenje je dovelo do morfoloških promjena osobito u povećanju lista, sjemenki, boji i uzorku sjemenki, prilgodbama u odnosu na promjene u fotoperiodu i sl.
- identificirano je 1835 gena kod srednjeameričkog genskog skupa i 748 gena kod andskog genskog skupa povezanih s udomaćivanjem (manje od 10% zajedničkih) (Schmutz i sur. 2014)

- raznolikost sekvenci pet različitih gena u divljim populacijama (*Bittochi i sur.* 2012; 2013):

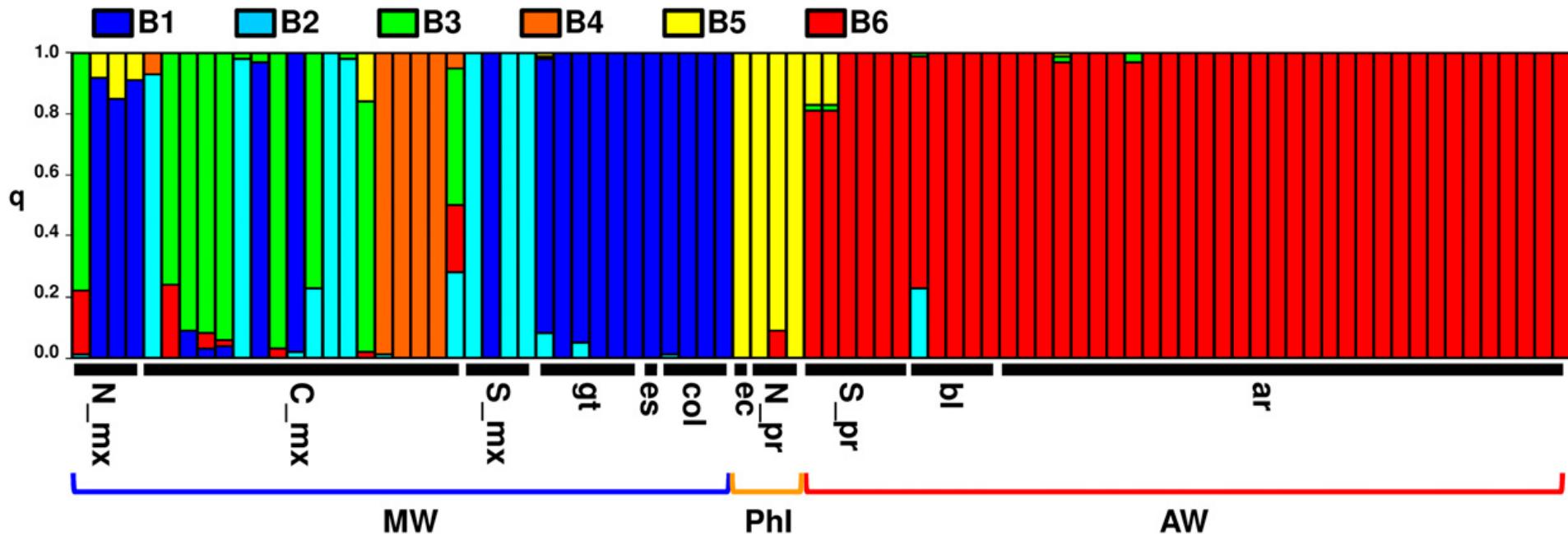
*leg044* - histidinol hidrogenaza

*leg100* – biotin sintetaza

*leg133* - dolicil-difosfooligosaharid protein glikoltransferaze,

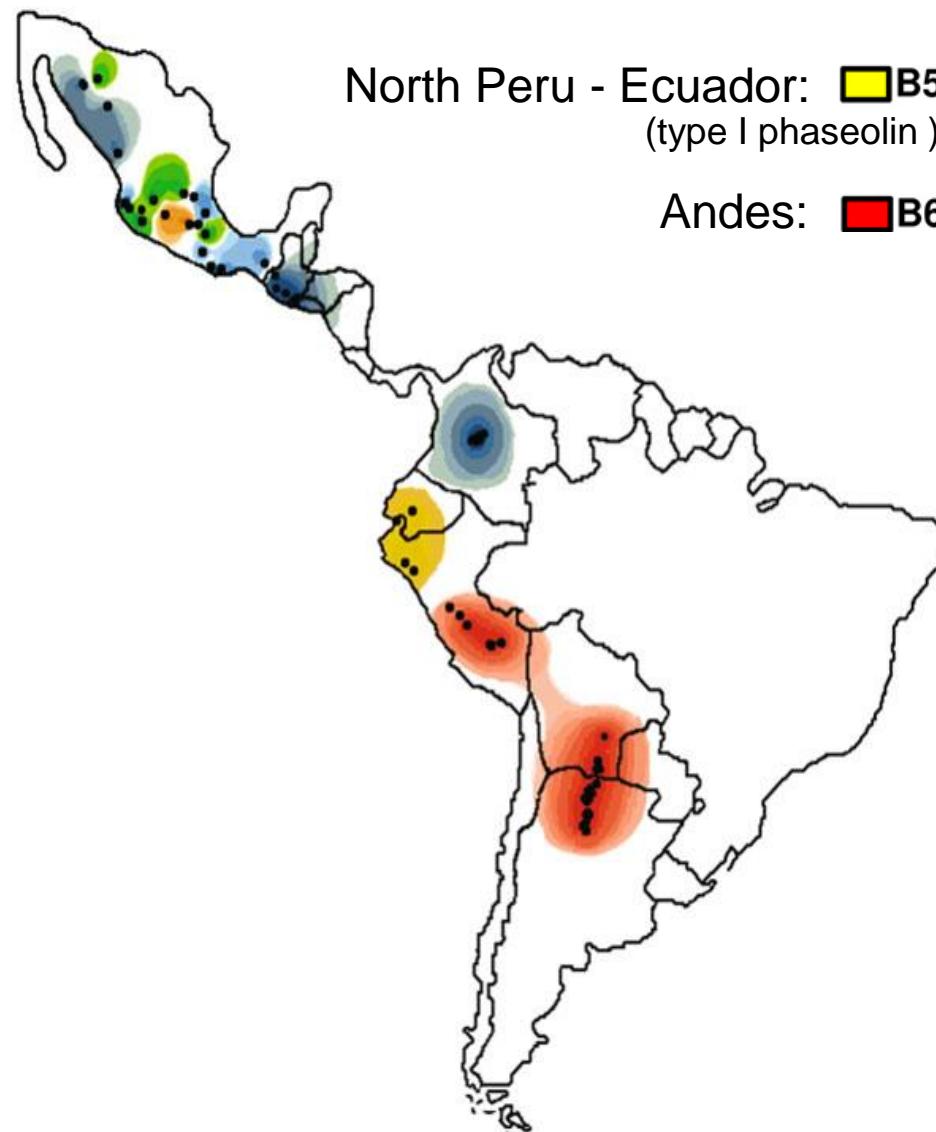
*leg 223* - translacijski inicijacijski faktor SUI1

*PvSHP1* - kontrola otvaranja ploda



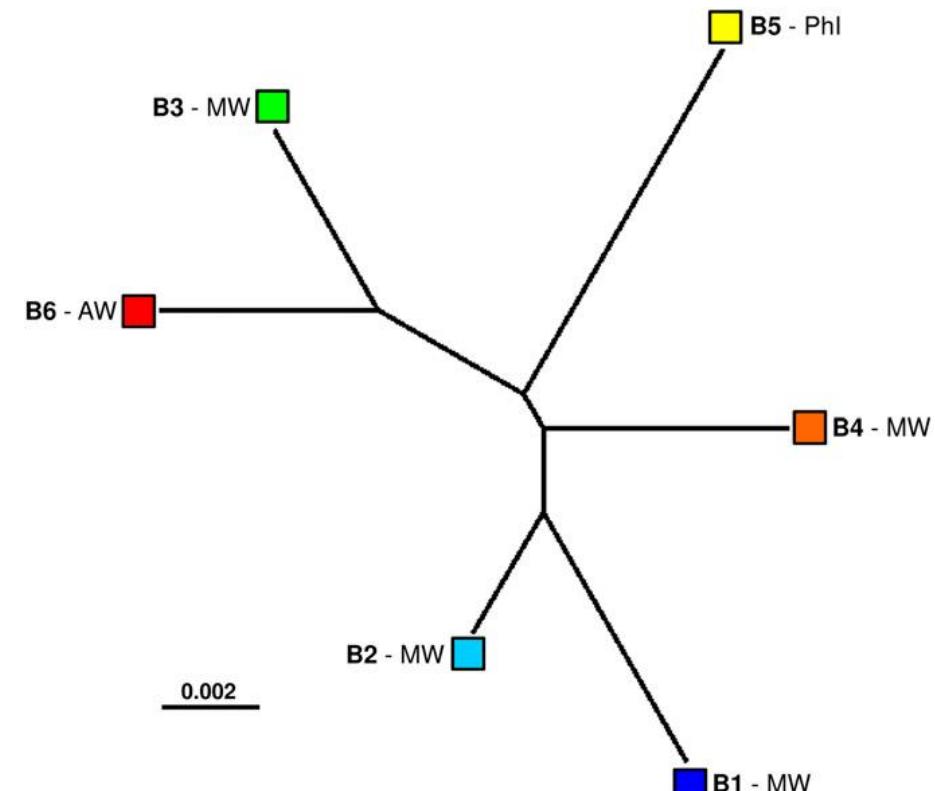
**Populacijsko genetička struktura (Bayesovski pristup, BAPS 5.3.)** (AW, Andean wild; ar, Argentina; bl, Bolivia; C\_mx, central Mexico; col, Colombia; ec, Ecuador; es, El Salvador; gt, Guatemala; MW, Mesoamerican wild; N\_mx, north Mexico; N\_pr, northern Peru; PhI, type I phaseolin (northern Peru–Ecuador); S\_mx, south Mexico; S\_pr, southern Peru).

Mesoamerica: B1 B2 B3 B4



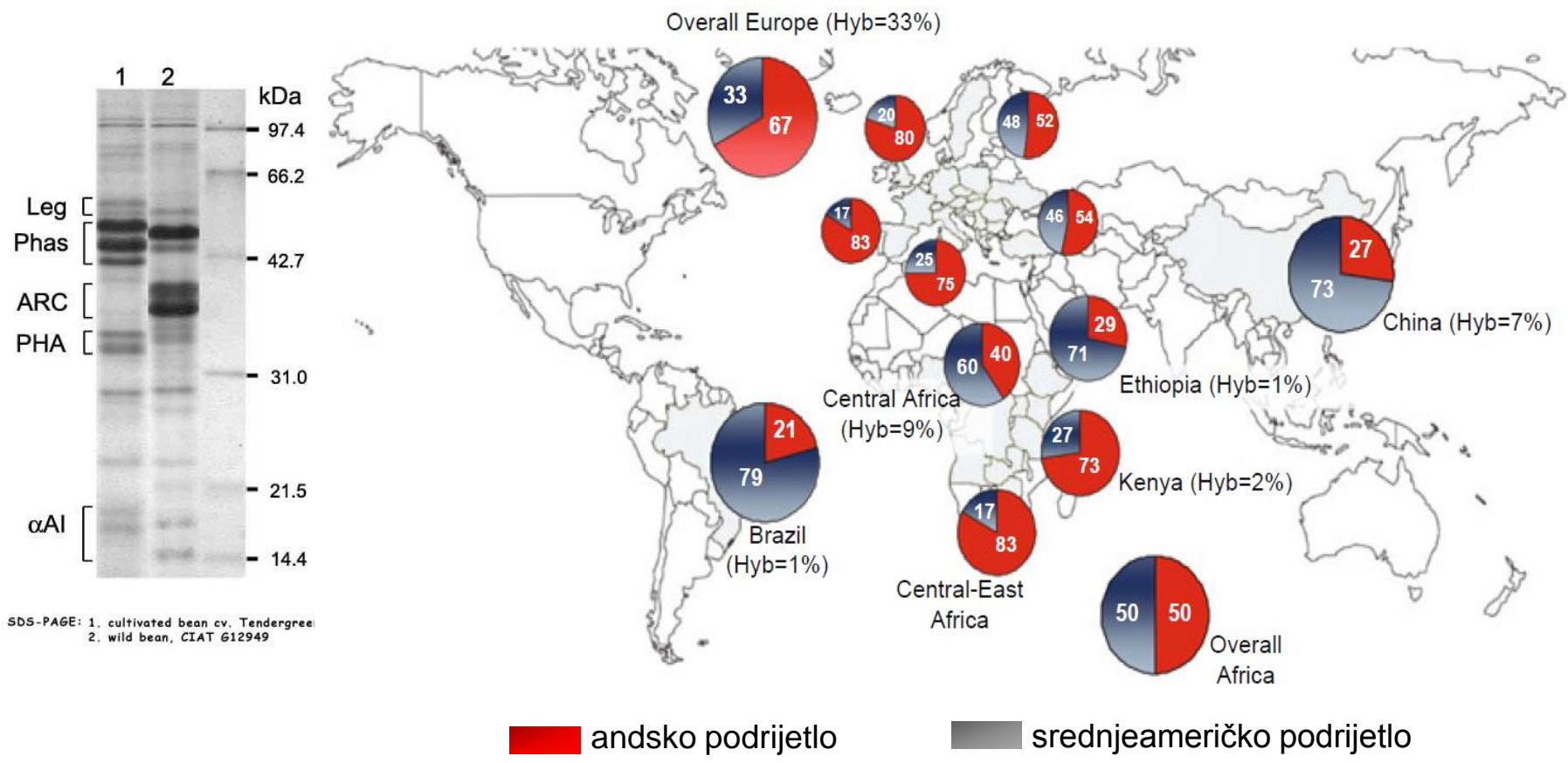
North Peru - Ecuador: B5  
(type I phaseolin)

Andes: B6



**Nezakorjenjeno srodstvenao NJ stablo**  
temeljeno na raznolikosti sekvenca pet jezgrenih  
lokusa

- putovi širenja graha izvan centara udomaćenja su vrlo kompleksni
- fazeolin je glavni spremišni protein u sjemenkama graha kodiran malom porodicom blisko smještenih gena
- prve studije su upotrebljavale izolaciju fazeolina iz sjemenki i SDS-PAGE elektroforezu kako bi razdvojili fazeolinske podjedinice i po njima razlikovali srednjeameričko od andskog podrijetla



prema Bellucci i sur. 2014

- konstruirane su PCR početnice unutar genske porodice za fazeolin koje umnožavaju mesta s 15 i 21-bp duplikacijama specifičnih kombinacija ovisno o geografskom podrijetlu (srednjeameričkom /S tipovi/ ili andskom /T tipovi/) (Kami 1995)

- u sjevernom Peru i Ekvadoru su pronađene populacije divljeg graha kojima potpuno nedostaju duplirane 15 i 21-bp regije (evolucijski najstariji tip fazeolina, I ili Inka tip)

#### Exon 3 → Intron 3

##### 21 bp repeat

I	TTCAATGTAAGAAAGAAAAACAGGCATCTAACACTACATAATTGGCGT.....
T1	TTCAATGTAAGAAAGAAAAACAGGCATCTAACACTACATAATTGGCGT.....
S1	TTCAATGTAAGAAAGAAAAACAGGCATCTAACACTACATAATTGGCGT.....
T2	TTCAATGTAAGAAAGAAAAACAGGCATCTAACACTACATAATTGGCGT.....
S2	TTCAATGTAAGAAAGAAAAACAGGCATCTAACACTACATAATTGGCGT.....
T3	TTCAATGTAAGAAAGAAAAACAGGCATCTAACACTACATAATTGGCGT.....

##### 15 bp repeat

I	GGAGATCAACAGGGTTCTGTTGAAGAGGAGGGACAGCAAGAGG.....
T1	GGAGATCAACAGGGTTCTGTTGAAGAGGAGGGACAGCAAGAGG.....
S1	GGAGATCAACAGGGTTCTGTTGAAGAGGAGGGACAGCAAGAGG.....
T2	GGAGATCAACAGGGTTCTGTTGAAGAGGAGGGACAGCAAGAGGAGGGACACGA.....
S2	GGAGATCAACAGGGTTCTGTTGAAGAGGAGGGACAGCAAGAGG.....
T3	GGAGATCAACAGGGTTCTGTTGAAGAGGAGGGACAGCAAGAGGAGGGACAGCA.....

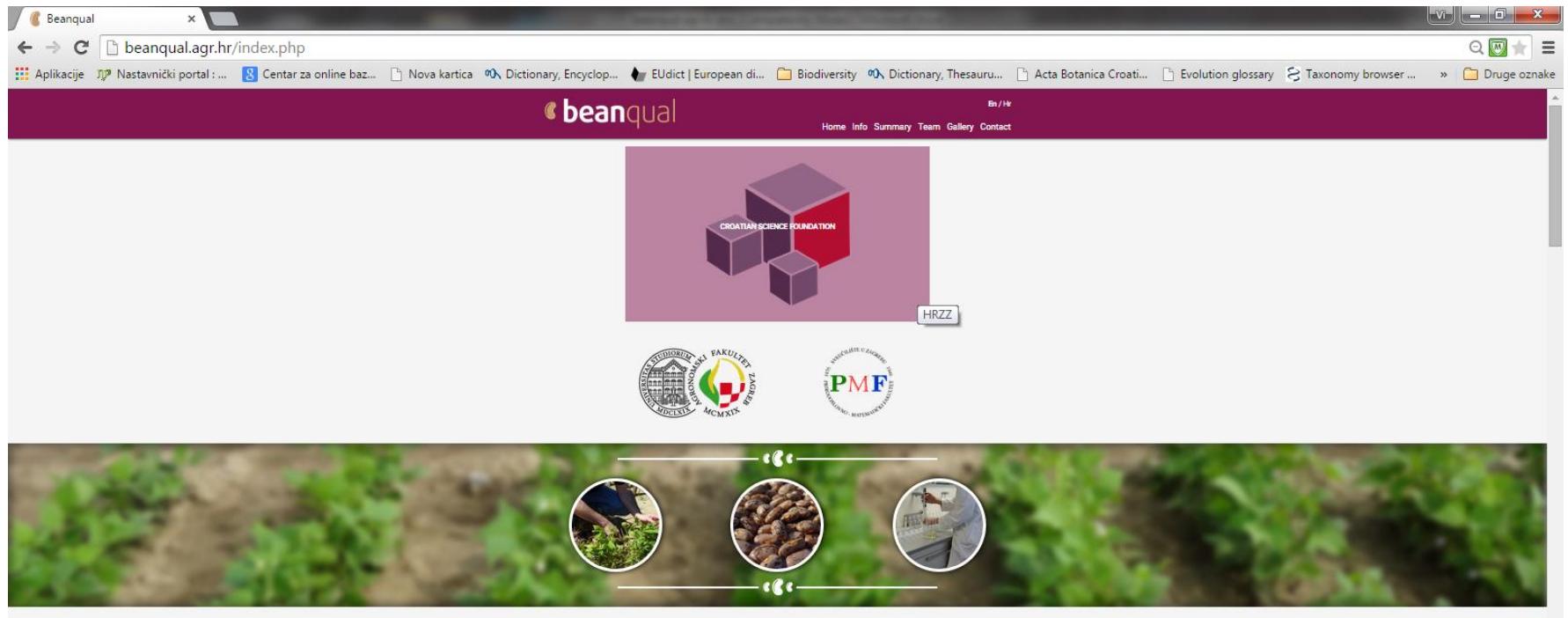
I	.....TGCCATTTAGCTAGTACTTTGTCTAAATGTCACACTTGGTTGAAT
T1	.....TGCCATTTAGCTAGTACTTTGTCTAAATGTCACACTTGGTTGAAT
S1	.....TGCCATTTAGCTAGTACTTTGTCTAAATGTCACACTTGGTTGAAT
T2	.....TGCCATTTAGCTAGTACTTTGTCTAAATGTCACACTTGGTTGAAT
S2	<u>ATATTTTGTGCCCCATTTAGCTAGTACTTTGTCTAAATGTCACACTTGGTTGAAT</u>
T3	<u>ATATTTTGTGCCCCATTTAGCTAGTACTTTGTCTAAATGTCACACTTGGTTGAAT</u>

I	.....GAGTGATTGTGAACATTGATTCT
T1	.....GAGTGATTGTGAACATTGATTCT
S1	.....GAGTGATTGTGAACATTGATTCT
T2	<u>AGAGGGAGTGATTGTGAACATTGATTCT</u>
S2	.....GAGTGATTGTGAACATTGATTCT
T3	<u>AGAGGGAGTGATTGTGAACATTGATTGT</u>

##### → Exon 4

I	TTGTTGAATGATATCATTATATGTTGCATGATTTTATAGAGCAAATTCGA
T1	TTGTTGAATGATATCATTATATGTTGCATGATTTTATAGAGCAAATTCGA
S1	TTGTTGAATGATATCATTATATGTTGCATGATTTTATAGAGCAAATTCGA
T2	TTTTTGAATGATATCATTATATGTTGCATGATTTTATAGAGCAAATTCGA
S2	TTGTTGAATGATATCATTATATGTTGCATGATTTTATAGAGCAAATTCGA
T3	TTGTTGAATGATATCATTATATGTTGCATGATTTTATAGAGCAAATTCGA

Phaseolin type	Fragment size (bp)				Origin
I tip	268	/	/	/	PhI
S tip	268	/	289	/	MA
T tip	268	283	/	304	AN



# **Genetic Basis of Bioactive Nutritient Content in Croatian Common Bean Landraces**

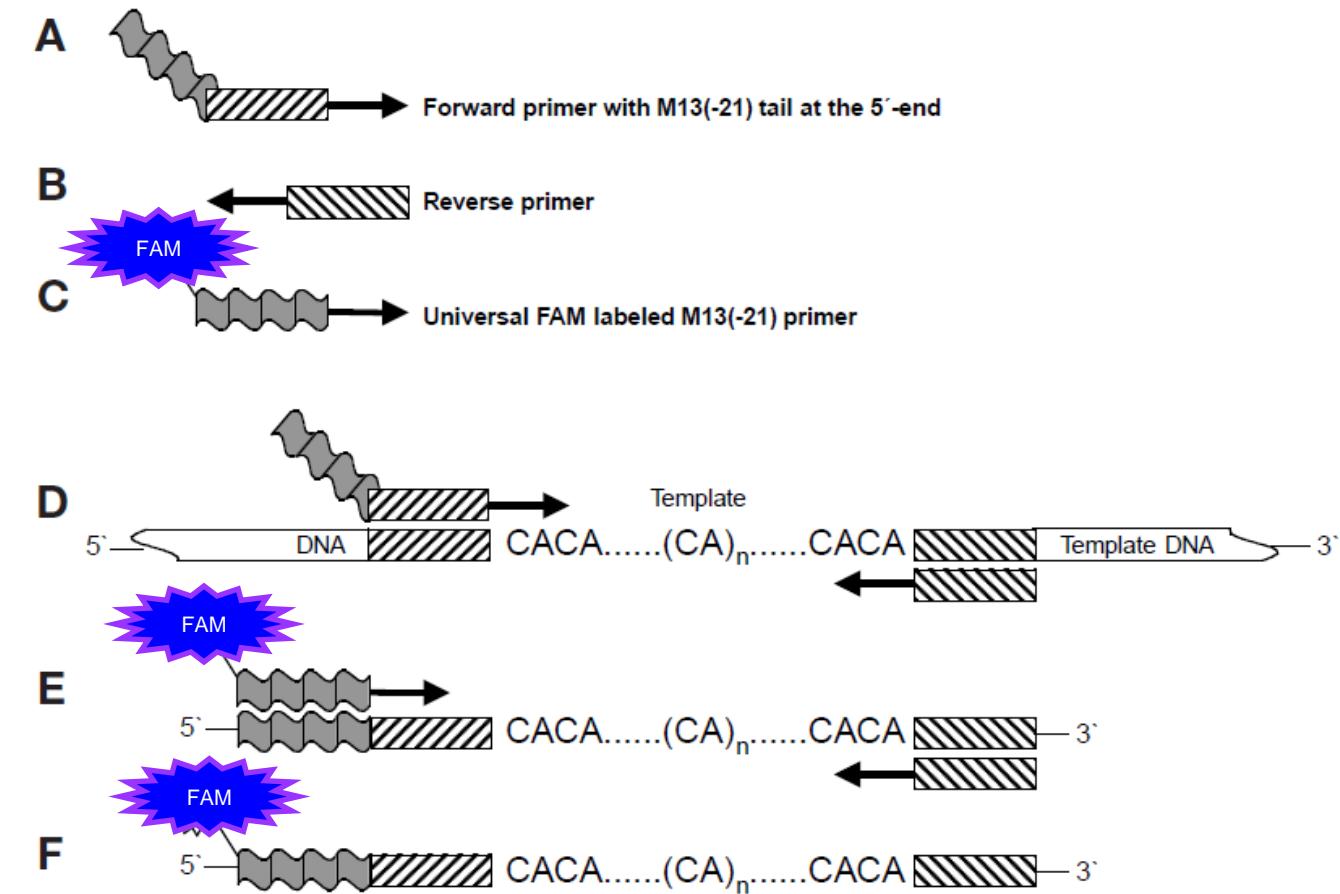
(1<sup>st</sup> of May 2014 - 30<sup>th</sup> of April 2017)

Doc. dr. sc. Klaudija Carović-Stanko  
Svaučilište u Zagrebu, Agronomski fakultet

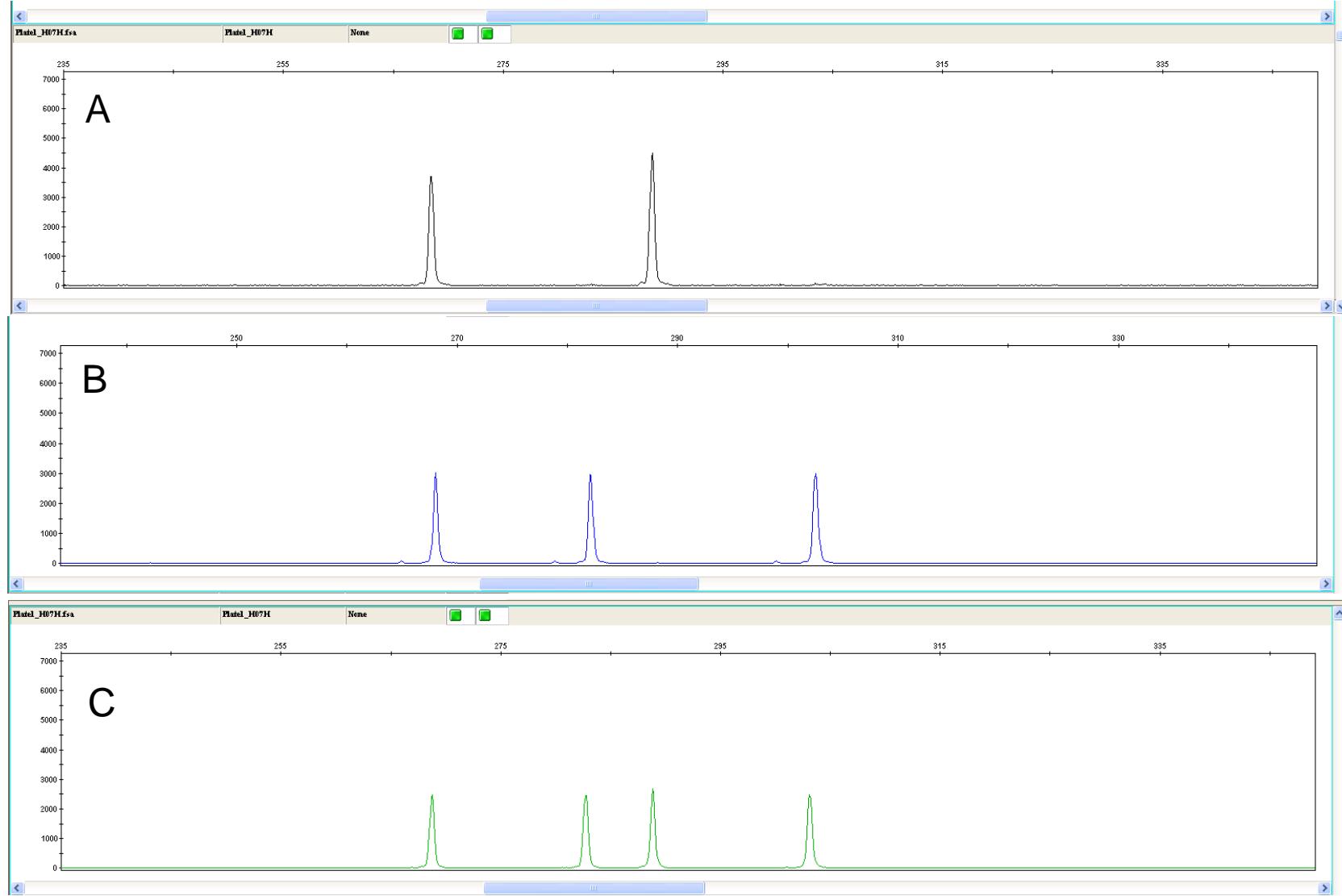
Objectives	Activities	Outputs – Milestones (M) and/or Deliverables (D)	Team members	Duration of activity (from-to, in months)
Multiplication and sampling	300 Croatian common bean landraces will be multiplied, leaf and seed samples sampled	Obtained material for analyses (D)	Klaudija Carović-Stanko Martina Grdiša Marko Petek Igor Palčić	from 2 <sup>nd</sup> to 6 <sup>th</sup> month
Yield potential assessment	Photosynthetic rates measurements	The assessment of diversity of 300 landraces (D)	Boris Lazarević Tomislav Karažija	from 3 <sup>rd</sup> to 5 <sup>th</sup> month
The assessment of diversity in seed mineral (Mg, Ca, Fe, Zn, K, P) and phytic acid content	Determination of Mg, Ca, Fe, Zn, K, P and phytic acid content	Material for association mapping and selection of interesting accessions (M) Data on seed mineral and phytic acid content (D)	Mirjana Herak Ćustić Marko Petek Igor Palčić Tomislav Karažija	from 7 <sup>th</sup> to 12 <sup>th</sup> month
DNA analysis	DNA extraction	DNA from 300 samples extracted and stored (D)	Klaudija Carović-Stanko Zlatko Liber Martina Grdiša Ivan Radosavljević	from 6 <sup>th</sup> to 9 <sup>th</sup> month
	Phaseolin type determination	Phaseolin type of 300 accessions determined (M)		from 9 <sup>th</sup> to 11 <sup>th</sup> month
	SSR markers	Amplification of DNA samples using 50 SSR markers (M); Fragment analysis (M); SSR marker data stored (D)		from 12 <sup>th</sup> to 17 <sup>th</sup> month
Construction of core collection	Selection of a subset representing 50% of whole collection	150 accessions selected for SNP analyses (D)	Klaudija Carović-Stanko Zlatko Liber Jerko Gunjača	from 18 <sup>th</sup> to 24 <sup>th</sup> month
DNA analysis	SNP markers	Whole genome variation characterization (M) Sup genotyping (D)	Contracted to a European Illumnia Certified Service provider	from 25 <sup>th</sup> to 27 <sup>th</sup> month
Data analyses	Genetic diversity and population structure evaluation; Association studies	Statistical data analyses (M); Interpretation of results (M); Results of the statistical analyses (D)	Klaudija Carović-Stanko Jerko Gunjača Zlatko Liber Marko Petek Boris Lazarević	from 22 <sup>nd</sup> to 36 <sup>th</sup> month

# An economic method for the fluorescent labeling of PCR fragments

(Schuelke 2000)

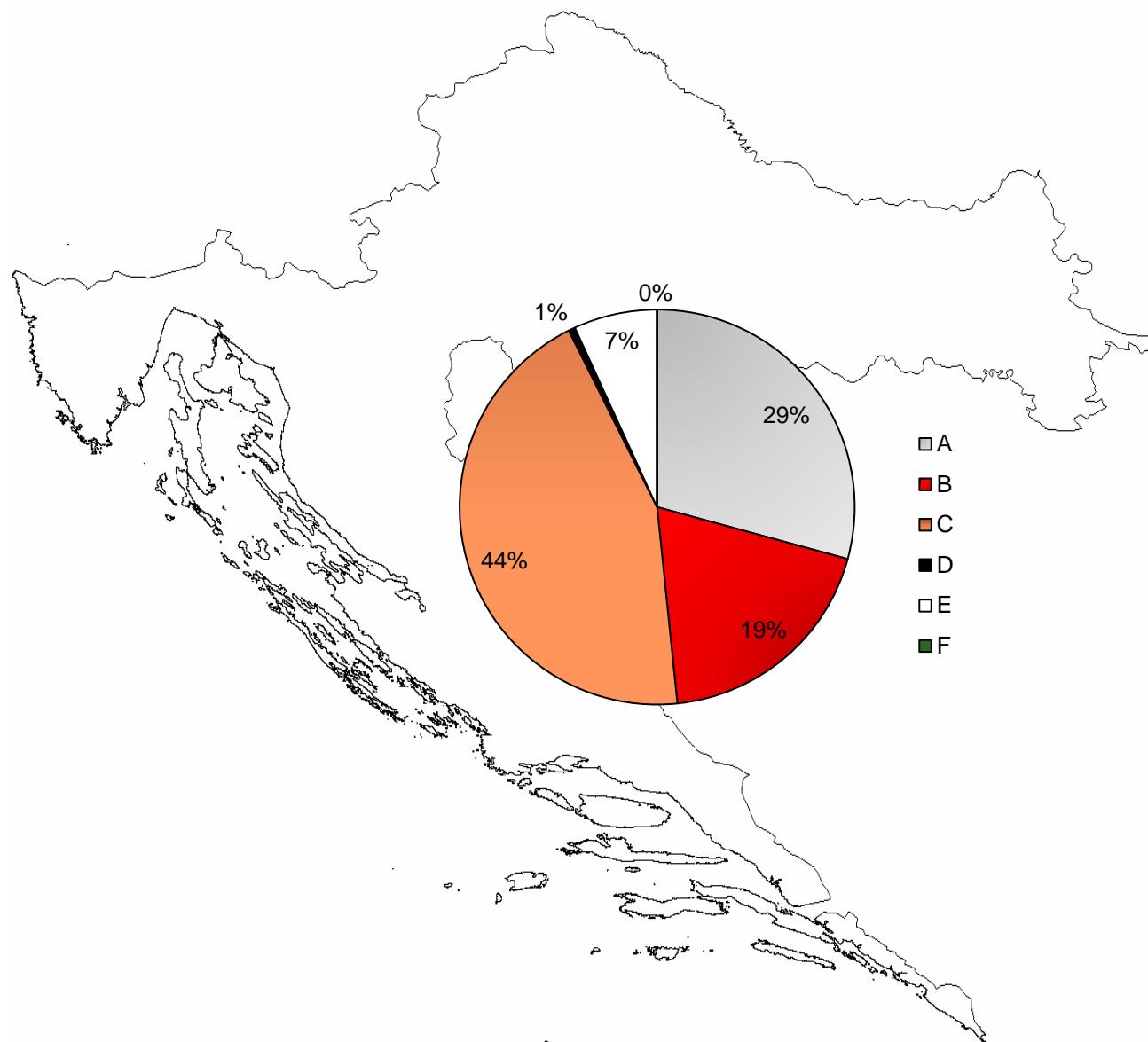


VIC  
NED  
PET



Phaseolin type	Fragment size (bp)			
A	268	/	289	/
B	268	283	/	304
C	268	283	289*	304

## Fazeolin tip hrvatskih tradicijskih kultivara graha





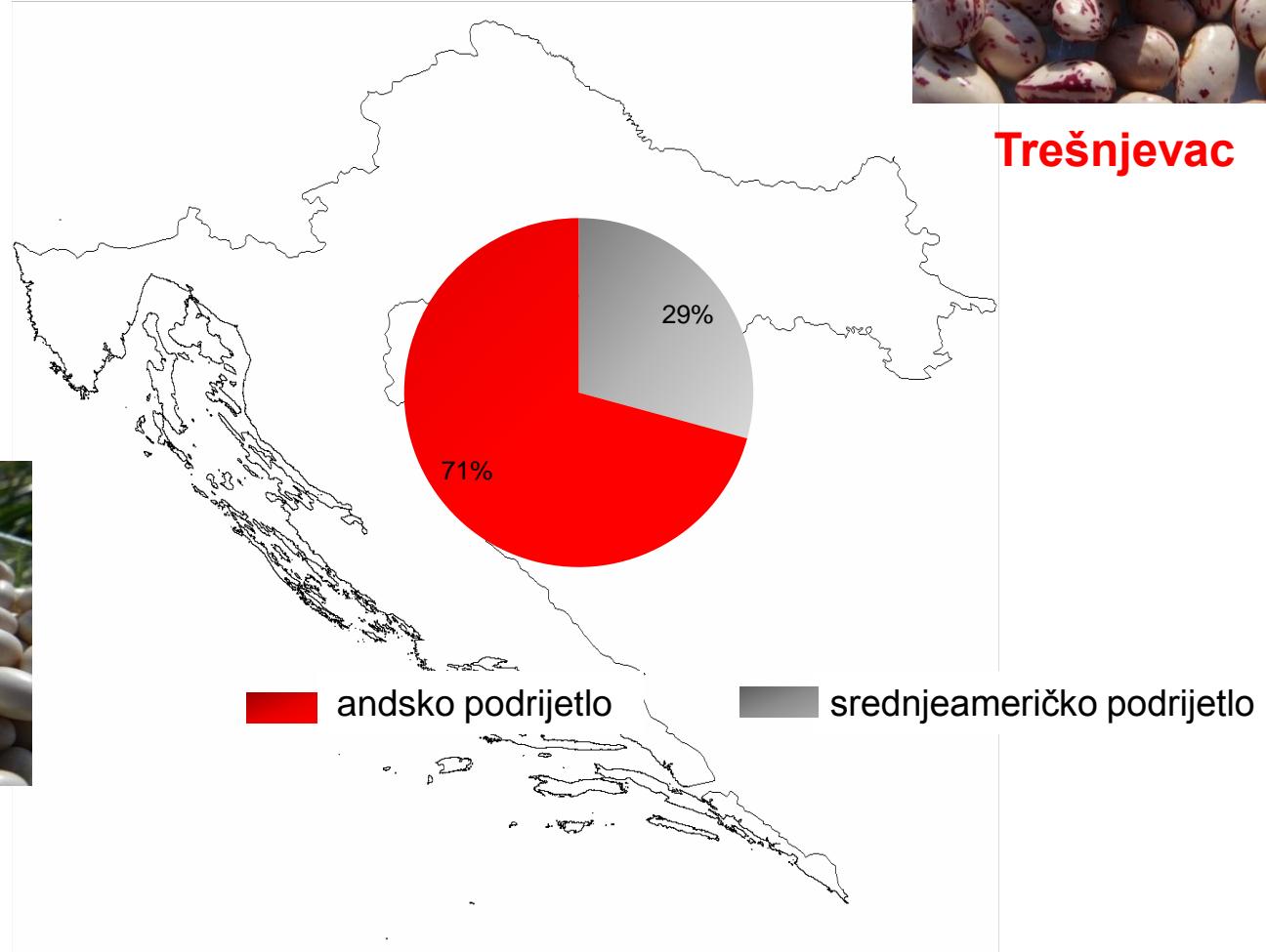
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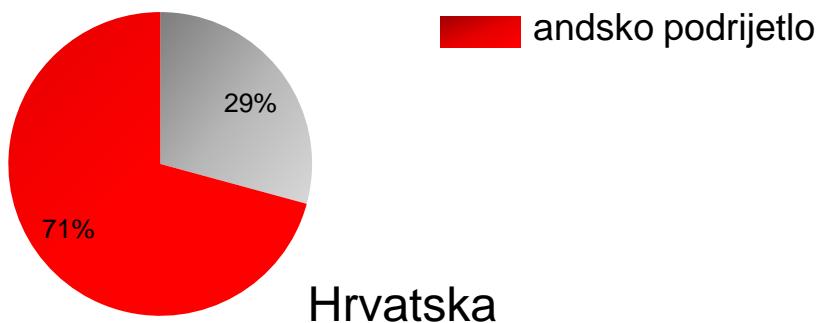
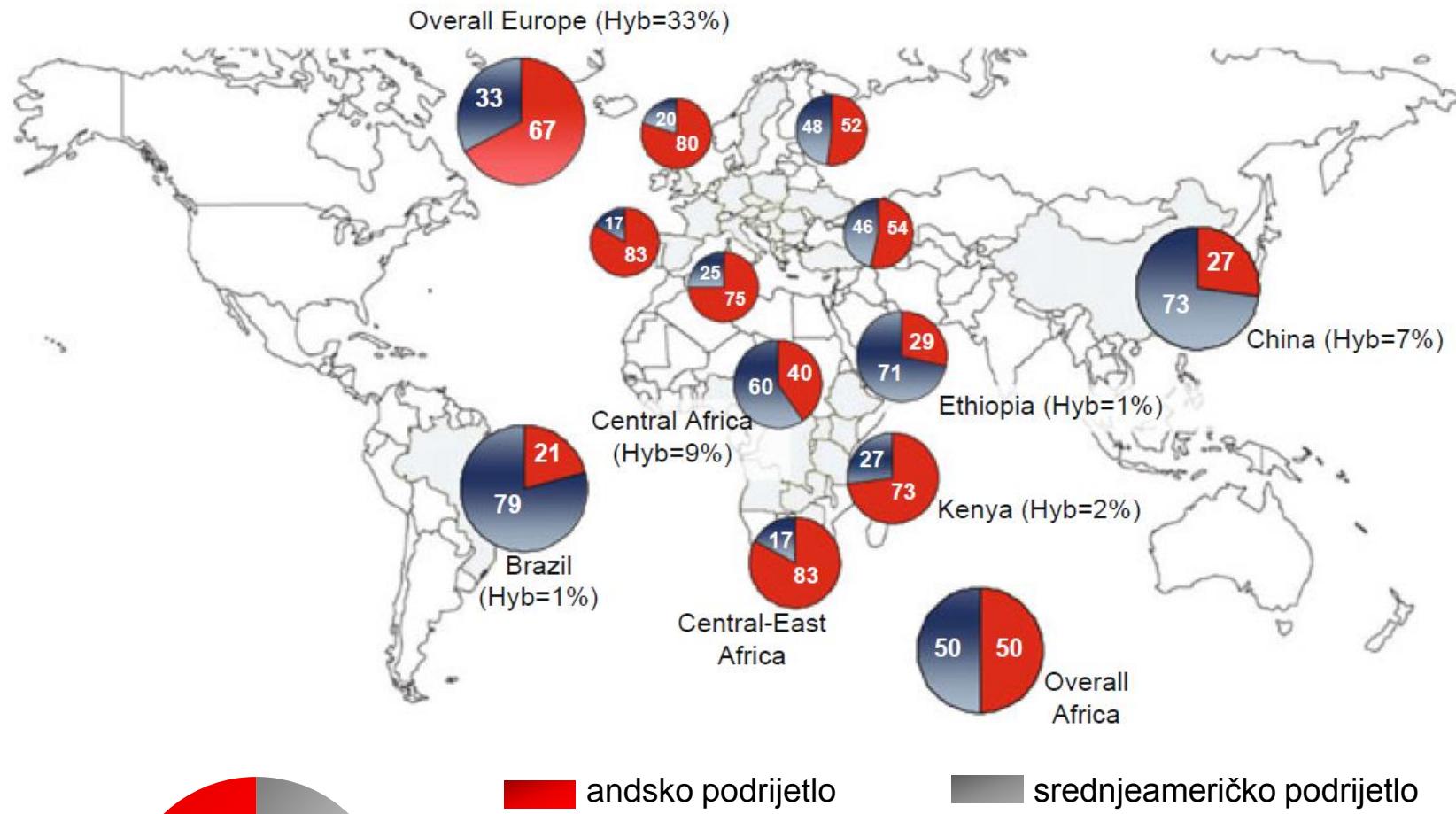


Biser



Trešnjevac





## LITERATURA

- Bellucci E. et al 2014. Genomics of Origin, Domestication and Evolution of *Phaseolus vulgaris*. U R Tuberosa, A Graner, E Frison (eds.): Genomics of Plant Genetic Resources, 483-507, Springer Netherlands, ISBN: 978-94-007-7571-8.
- Bitocchi E, Nanni L, Bellucci E et al et al. 2012. Mesoamerican origin of the common bean (*Phaseolus vulgaris* L.) is revealed by sequence data. *Proc Natl Acad Sci U S A*: e788–e796.
- Bitocchi E, Bellucci E, Giardini A et al 2013. Molecular analysis of the parallel domestication of the common bean in Mesoamerica and the Andes. *New Phytol* 197:300–313.
- Delgado-Salinas A, Bibler R, Lavin M 2006. Phylogeny of the genus *Phaseolus* (Leguminosae): a recent diversification in an ancient landscape. *Syst Bot* 31:779–791
- Gaut B. S. 2014. The complex domestication history of the common bean. *Nature Genet* 46 (7):663-664.
- Kami J, Becerra-Velásquez V, Debouck DG et al 1995. Identification of presumed ancestral DNA sequences of phaseolin in *Phaseolus vulgaris*. *Proc Natl Acad Sci U S A* 92:1101–1104.
- Kwak M, Gepts P 2009. Structure of genetic diversity in the two major gene pools of common bean (*Phaseolus vulgaris* L., Fabaceae). *Theor Appl Genet* 118:979–992.
- Rossi i sur. 2009. Linkage disequilibrium and population structure in wild and domesticated populations of *Phaseolus vulgaris* L. *Evol Appl* 2:504–522.

Schuelke, M. 2000. An economic method for fluorescent labeling of PCR fragments. *Nat Biotechnol* 18: 233–234.

Schmutz J. et al. 2014. A reference genome for common bean and genome-wide analysis of dual domestications. *Nat Genet* 46 (7): 707–713.